

App #: 09/675, 650

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 08:17:56 ; Search time 1513 Seconds  
(without alignments)  
7516.772 Million cell updates/sec

Title: US-09-675-650-2  
Perfect score: 278  
Sequence: 1 caggaagcaaaaaggaagc.....ggtccacaagacatgcaac 278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
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- 12: gb\_sy:\*
- 13: gb\_un:\*
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- 16: em\_fun:\*
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- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	100.0	278	6	AX107858
2	266	95.7	812	6	AR261039 Sequence
3	266	95.7	812	6	AR278570 Sequence
4	266	95.7	812	6	AX106207 Sequence
5	266	95.7	812	6	AX106690 Sequence
6	266	95.7	812	6	AX140981 Sequence
7	266	95.7	812	6	AX200841 Sequence
8	266	95.7	812	6	AX267497 Sequence
9	266	95.7	812	6	BD082484 PCA3, PCA
10	266	95.7	1872	6	BD082483 PCA3, PCA
11	266	95.7	2037	6	BD082482 PCA3, PCA
12	266	95.7	2229	6	AR261037 Sequence
13	266	95.7	2229	6	AR278568 Sequence
14	266	95.7	2229	6	AX106205 Sequence
15	266	95.7	2229	6	AX106688 Sequence
16	266	95.7	2229	6	AX140979 Sequence
17	266	95.7	2229	6	AX200839 Sequence
18	266	95.7	2229	6	AX267495 Sequence
19	266	95.7	2229	6	AR261038 Sequence
20	266	95.7	2229	6	AR278569 Sequence
21	266	95.7	2229	6	AX106206 Sequence
22	266	95.7	2229	6	AX106689 Sequence
23	266	95.7	2229	6	AX140980 Sequence
24	266	95.7	2229	6	AX200840 Sequence
25	266	95.7	2229	6	AX267496 Sequence
26	266	95.7	2229	6	AR261036 Sequence
27	266	95.7	2229	6	AR278567 Sequence
28	266	95.7	2229	6	AX106204 Sequence
29	266	95.7	2229	6	AX106687 Sequence
30	266	95.7	2229	6	AX140978 Sequence
31	266	95.7	2229	6	AX200838 Sequence
32	266	95.7	2229	6	AX267494 Sequence
33	266	95.7	2229	6	BD082485 PCA3, PCA
34	266	95.7	2229	6	AR261166 Sequence
35	266	95.7	2229	6	AR278697 Sequence
36	266	95.7	2229	6	AX200988 Sequence
37	266	95.7	2229	6	AX267716 Sequence
38	266	95.7	2229	6	AF103907 Homo sapi
39	255.4	91.9	506	6	AX107857 Sequence
40	243.4	87.6	5435	9	AF103908 Homo sapi
41	243.4	87.6	128480	9	AL359314 Human DNA
42	241	86.7	718	6	AR237401 Sequence
43	241	86.7	718	6	AR260894 Sequence
44	241	86.7	718	6	AR278425 Sequence
45	241	86.7	718	6	AX106203 Sequence

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
AX107858	AX107858	Sequence 2 from Patent WO0123550.	AX107858	AX107858.1	GI:13923250		Homo sapiens (human)	Busse, U., Chypre, C. and Fradet, Y.
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Pca3 messenger rna species in benign and malignant prostate tissues
								Patent: WO 0123550-A 2 05-APR-2001;

Diagnocure Inc. (CA)										
FEATURES	Source	Location/Qualifiers								
		1..278								
		/organism="Homo sapiens"								
		/mol_type="genomic DNA"								
		/db_xref="taxon:9606"								
BASE COUNT	90 a	54 c	75 g	59 t						
ORIGIN										
Query Match	100.0%	Score 278;	DB 6;	Length 278;						
Best Local Similarity	100.0%	Pred. No. 4.6e-72;								
Matches 278;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
Qy	1	CAGGAGACAAAAGGAGACACAGATCCCTGGGAGAAATGCCCGGCGGCATCTGGG	60							
Db	1	CAGGAGACAAAAGGAGACACAGATCCCTGGGAGAAATGCCCGGCGGCATCTGGG	60							
Qy	61	TCATGATGACCTCGCCCTGCTGCTGCTGCTGAGGAGAACATTAGAAATG	120							
Db	61	TCATGATGACCTCGCCCTGCTGCTGCTGCTGAGGAGAACATTAGAAATG	120							
Qy	121	AATTGATGTCTCTTAAAGATGGGACAGAAACAGATCCTGTTGGATATTATTG	180							
Db	121	AATTGATGTCTCTTAAAGATGGGACAGAAACAGATCCTGTTGGATATTATTG	180							
Qy	181	AACGGATTACAGATTGAAATGAAAGTACCAAATGACATTACATGAGAGAAAC	240							
Db	181	AACGGATTACAGATTGAAATGAAAGTACCAAATGACATTACATGAGAGAAAC	240							
Qy	241	AGACGAGAAATCTGTATGCTTCAAGACATGCAAC	278							
Db	241	AGACGAGAAATCTGTATGCTTCAAGACATGCAAC	278							

LOCUS	AR261039	812 bp	DNA	linear	PAT 29-JAN-2003
DEFINITION	Sequence	471	from patent	US 6321716.	
ACCESSION	AR261039				
VERSION	AR261039.1	GI:28071802			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 812)				
TITLE	Mashiki, Z. and Harada, J.				
JOURNAL	Negative pressure control apparatus for engine mounted in vehicle				
FEATURES	Patent: US 6321716-A 471 27-NOV-2001;				
	Location/Qualifiers				
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	/organism="unknown"				
BASE COUNT	198 a	189 c	169 g	256 t	
ORIGIN					
Query Match	95.7%;	Score 266;	DB 6;	Length 812;	
Best Local Similarity	99.6%;	Pred. No. 2e-66;			
Matches 277;	Conservative	0;	Mismatches	0;	Indels 1;
					Gaps 1;
Db	1	CAGGAAGCACAAAAGGAGGACACAGAGATCCCTGGGAGAAATGCCGGCGGCATCTTGGG	60		
Db	562	CAGGAAGCACAAAAGGAGGACACAGAGATCCCTGGGAGAAATGCCGGCGGCATCTTGGG	503		
Db	61	TCATGATGAGCCTCGCCCTGCTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG	120		
Db	502	TCATGATGAGCCTCGCCCTGCTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG	443		
Db	121	AATTGATGTGTTCTCTTAAAGATGGGCGAGAAAACAGATCCTGTGTGATATTATTG	180		
Db	442	AATTGATGTGTTCTCTTAAAGATGGGCGAGAAAACAGATCCTGTGTGATATTATTG	383		
Db	181	AACGGGATTACGATTTGAAATGAAAGTCACCAAAAGTGACATTACCATGAGAGGAAAC	240		
Db	382	AACGGGATTACGATTTGAAATGAAAGTCA-CAAAGTGACATTCACCAATGAGAGGAAAC	324		

QY	241	AGACGAGAAATCTTGATGGCTTCACAGCATGCACAC	278
Db	323	AGACGAGAAATCTTGATGGCTTCACAGCATGCACAC	286
RESULT 3			
LOCUS	AR278570/c		
DEFINITION	AR278570	812 bp	DNA
ACCESSION	Sequence	471 from patent US 6512094.	linear
VERSION	AR278570		
KEYWORDS	AR278570.1	GI:29712816	
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 812)		
	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,		
	Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,		
	Weplick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,		
	Heppler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate		
	Cancer		
JOURNAL	Patent: US 6512094-A 471, 28- <del>JAN</del> -2003;		
FEATURES	Location/Qualifiers		
source	1..812		
	/organism="unknown"		
BASE COUNT	198 a 189 c 169 g 256 t		
ORIGIN			
Query Match	95.7%;	Score 266;	DB 6;
Best Local Similarity	99.6%;	Pred. No. 2e-68;	Length 812;
Matches 277;	Conservative	0;	Mismatches 0;
		Indels 1;	Gaps 1;

Oy		1	CAGGAACCAAAAAAGAGAACAAGATCCCTGGGAAATAAGCCCGGCCCATCTTGGG	60
Dd		562	CAGGAACCAAAAAAGAGAACAAGATCCCTGGGAAATAAGCCCGGCCCATCTTGGG	503
Oy		61	TCATCGATGAGCCTCGCCCTGTGCCTTGCTCCCTTTGTAGGGAGAGCATTTGAAAATG	120
Dd		502	TCATCGATGAGCCTCGCCCTGTGCCTTGCTCCCTTTGTAGGGAGAGCATTTGAAAATG	443
Oy		121	AATTGATGTAATTCCTTAAAGATGGGAGGAAAAACAATCCTGTGTGGATATTATTGG	180
Dd		442	AATTGATGTAATTCCTTAAAGATGGGAGGAAAAACAATCCTGTGTGGATATTATTGG	383
Oy		181	AACGGATTACAGATTGGAATGAAGTACCACCAAAGTAGCATTTACCAATGAGAGAAAC	240
Dd		382	AACGGATTACAGATTGGAATGAAGTACCACCAAAGTAGCATTTACCAATGAGAGAAAC	324
Oy		241	AGACGAGAAAAATCTTGATGCGCTTCACAAAGCATGCAAC	278
Dd		323	AGACGAGAAAAATCTTGATGCGCTTCACAAAGCATGCAAC	286
RESULT 4				
LOCUS	AX106207/c			
DEFINITION	Sequence 345 from Patent WO0125273.	812 bp	DNA	linear PAT 30-APR-2001
ACCESSION	AX106207			
VERSION	AX106207.1 GI:13921896			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Skely,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.			
JOURNAL	Compositions and methods for wtl specific immunotherapy			
FEATURES	Patent: WO 0125273-A 345 12-APR-2001;			
SOURCE	CORIXA CORPORATION (US)			
	Location/Qualifiers			
	I..812			





Oy	241	AGACGAGAAATCTTGATGGCTTCAACAAGATGCAC	278
Db	495	AGACGAGAAATCTTGATGGCTTCAACAAGATGCAC	532
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LOCUS	BD082483	1872 bp	DNA linear PAT 27-AUG-2002
DEFINITION	BD082483 PCAs genes, and methods of use.		
ACCESSION	BD082483.1 GI:22628093		
VERSION	JP 2001522240-A/2.		
KEYWORDS	Mastadenovirus		
SOURCE	Mastadenovirus		
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Adenoviridae.		
REFERENCE	1 (bases 1 to 1872)		
AUTHORS	Bussemakers,M,J.G.		
TITLE	PCAs, PCAs genes, and methods of use		
JOURNAL	Patent: JP 2001522240-A 2 13-NOV-2001;		
COMMENT	DIAGNOCURE INC		
	PB	JP 2001522240-A/2	
	PD	13-NOV-2001	
	PF	09-APR-1998 JP 1998542194	
	PR	10-APR-1997 US 60/041836	
	PI	MARTON J G, BUSSEMAKERS	
	PC	CI2NI5/00, CI2NI5/12, CI2NI5/12, CI2NI/21, COTKI4/47, COTKI6/18, PC	
		CI2QI/68,	
	PC	G01N3/577, A61K39/395, A01K67/027	
	CC	Strandedness: Double;	
	CC	Topology: Linear;	
FEATURES			
source	Location/Qualifiers		
	1..1872		
	/organism="Mastadenovirus"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:10509"		
BASE COUNT	567 a 389 c 369 g 539 t 8 others		
ORIGIN			
Query Match	95.7%; Score 266; DB 6; Length 1872;		
Best Local Similarity	99.6%; Pred. No. 2,2e-68;		
Matches 277; Conservative	0; Mismatches 0; Indels 1; Gaps 1;		
Oy	1	CAGAGAAGCAGAAAAGAGAAGCAGAGATCCCTGGAGGAATGCCCGGCCCATCTTTGGG	60
Db	256	CAGAGAAGCAGAAAAGAGAAGCAGAGATCCCTGGAGGAATGCCCGGCCCATCTTTGGG	315
Oy	61	TCATGATGAGCCCTGCGCTGTGCTGCTCCCGCTTGTGAGGAAAGCATTAGAAAAATG	120
Db	316	TCATGATGAGCCCTGCGCTGTGCTGCTCCCGCTTGTGAGGAAAGCATTAGAAAAATG	375
Oy	121	AATTGATGTGTTCTCTTAAGATGTGGGAGAAAACAGATCCCTGTTGTGATATTATTATTTG	180
Db	376	AATTGATGTGTTCTCTTAAGATGTGGGAGAAAACAGATCCCTGTTGTGATATTATTATTTG	435
Oy	181	AACGGGATTACAGATTGAAAAAGTAGAAGTCAACCAAAAGTGAATTCATTCATGAGAGAAAAAC	240
Db	436	AACGGGATTACAGATTGAAAAAGTAGAAGTCA-CAAAGTGAATTCATTCATGAGAGAGAAAAAC	494
Oy	241	AGACGAGAAATCTTGATGGCTTCAACAAGATGCAC	278
Db	495	AGACGAGAAATCTTGATGGCTTCAACAAGATGCAC	532
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RESULT 11			
LOCUS	BD082482	2037 bp	DNA linear PAT 27-AUG-2002
DEFINITION	PCAs, PCAs genes, and methods of use.		
ACCESSION	BD082482.1 GI:22628092		
VERSION	JP 2001522240-A/1.		
KEYWORDS	Mastadenovirus		
SOURCE	Mastadenovirus		
ORGANISM	Mastadenovirus		

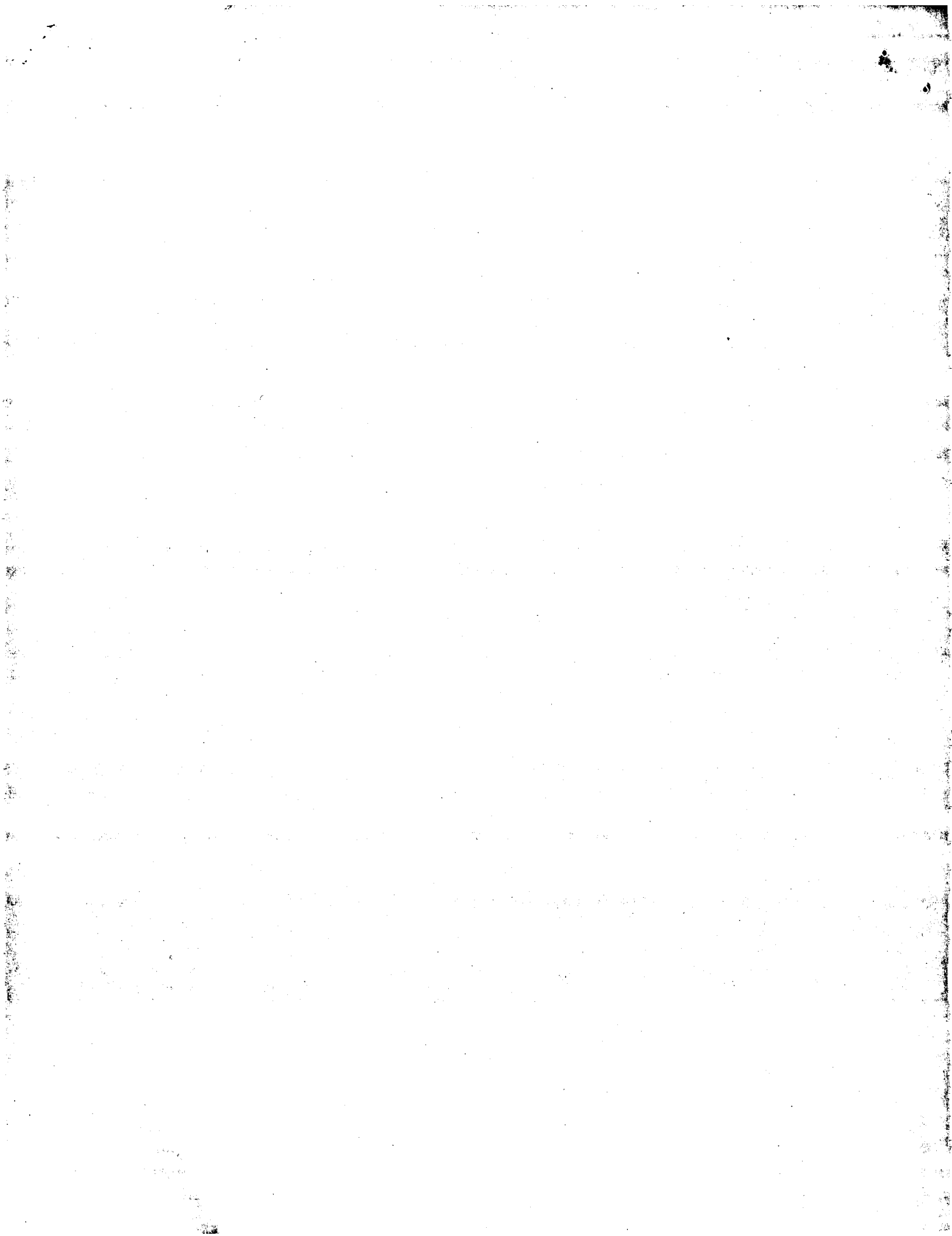
REFERENCE	1 (bases 1 to 2037)			
AUTHORS	Bussemakers, M.U.G.			
TITLE	PCa3, PCa3 genes, and methods of use			
JOURNAL	Patent: JP 2001522240-A 13-NOV-2001; DIAGNOSTIC INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES			
COMMENT	PN JP 2001522240-A/1 PD 13-NOV-2001 PF 09-APR-1998 JP 1998542194 PR 10-APR-1997 US 60/041836 PI MARION J G BUSSEMAKERS PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC C1201/68. PC G01N33/577, A61K39/395, A01K67/027 CC Strandedness: Doublet; CC Topology: Linear; FH Key Location/Qualifiers FT CDS 379..531.			
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ORIGIN	6 others			
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Best Local Similarity	99.6%;	Pred. No. 2.2e-68;		
Matches 277;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1 CAGGAACACAAAGAAGACACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGG 60			
DB	421 CAGGAAGACAAAGAAGACACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGG 480			
QY	61 TCATCGATGAGACCTCGCCCTTGCTGCTGATCCCGCTTGAGAGGAAGACATTAGAAATG 120			
DB	481 TCATCGATGAGACCTCGCCCTTGCTGCTGATCCCGCTTGAGAGGAAGACATTAGAAATG 540			
QY	121 AATTGATGTGTTCTTAAAGGATGGGACGAGAAAACAATCCTGTGTGATATTATTG 180			
DB	541 AATTGATGTGTTCTTAAAGGATGGGACGAGAAAACAATCCTGTGTGATATTATTG 600			
QY	181 AACGGATTACAGATTGGAATGAATGATGACCAAGTGAAGTTCATGAGAGGAAAC 240			
DB	601 AACGGATTACAGATTGGAATGAAGTGAAGTTCATGAGAGGAAAC 659			
QY	241 AGACGAGAAATCTTGATGCTTACACAGACATGCAAC 278			
DB	660 AGACGAGAAATCTTGATGCTTACACAGACATGCAAC 657			
RESULT 12				
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LOCUS	Sequence 469 from patent US 6321716.			
DEFINITION	AR261037			
ACCESSION	AR261037.1 GI:28071800			
VERSION				
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 2229)			
AUTHORS	Mashiki, Z. and Harada, J.			
TITLE	Negative pressure control apparatus for engine mounted in vehicle			
JOURNAL	Patent: US 6321716-A 469 27-NOV-2001;			
FEATURES	Location/Qualifiers 1..2229 /organism="unknown"			
BASE COUNT	654 a	447 c	481 g	647 t
ORIGIN				
Query Match	95.7%	Score 266;	DB 6;	Length 2229;
Best Local Similarity	99.6%;	Pred. No. 2.2e-68;		



Query Match 95.7%; Score 266; DB 6; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 2.2e-68;  
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	CAGGAAGCCAAAGAGAGACAGAGATCCCTGGAGAAATGCCCGCCGCCATCTTGGG	60
Db	1617	CAGGAAGCCAAAGAGAGACAGAGATCCCTGGAGAAATGCCCGCCGCCATCTTGGG	1558
QY	61	TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG	120
Db	1557	TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG	1498
QY	121	AATTGATGTGTCCTTAAGAGATGGCGAGAAAAACAGATCCTGTGTGATATTATTG	180
Db	1497	AATTGATGTGTCCTTAAGAGATGGCGAGAAAAACAGATCCTGTGTGATATTATTG	1438
QY	181	AACGGATTACAGATTGAAATGAGTCACCAAGTGAGCATTACCAATGAGAGAAAAC	240
Db	1437	AACGGATTACAGATTGAAATGAGTCACCAAGTGAGCATTACCAATGAGAGAAAAC	1379
QY	241	AGACGAGAAAATCTTGATGGCTTCACAAAGCATGCAAC	278
Db	1378	AGACGAGAAAATCTTGATGGCTTCACAAAGCATGCAAC	1341

Search completed: February 1, 2004, 10:18:49  
Job time : 1515 secs











QY	61	CAATGATGACCTGCGCCCTGTGCCTGGTCCCGCTGTGAGGAAAGACATTAGAAATG	120
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QY	121	AATTGATGTGTTCCCTTAAAGATGGGACAGAAACAGATCCGTGTGATATTATTG	180
Db	1591	AATTGATGTGTTCCCTTAAAGATGGGACAGAAACAGATCCGTGTGATATTATTG	1650
QY	181	AACGGGATTACAGATTTGAAATGAAAGTCACCAAAGTGCATTACCAATGAGAGAAAAC	240
Db	1651	AACGGGATTACAGATTTGAAATGAAAGTCA-CAAAGTGCATTACCAATGAGAGAGAAAAC	1709
QY	241	AGACGAGAAATCTTGATGGCTCCCAAGACACATGCAAC	278
Db	1710	AGACGAGAAATCTTGATGGCTCCCAAGACACATGCAAC	1747

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RESULT 8
US-09-352-616A-468
Sequence 468, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42768
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

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Query Match	95.7%	Score 266;	DB 4;	Length 3112;
Best Local Similarity	99.6%	Pred. No. 1.8e-79;		
Matches 277;	Conservative	0;	Mismatches 0;	Indels 1;
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Oy	1	CAGGAGACAAAAGGAGCACAAGAGATCCCTGGGAGAAATGCCCGGCGCATTTGGG	60
Db	1471	CAGGAGACAAAAGGAGCACAAGATCCCTGGGAGAAATGCCCGGCGCATTTGGG	1530
Oy	61	TCATCGATGAGCTCGCCCTGTGCTGGTCCCGCTTGTGAGGGANGACATTAGAAATG	120
Db	1531	TCATCGATGAGCCTCGCCCTGTGCTGGTCCCGCTTGTGAGGGANGACATTAGAAATG	1590
Oy	121	AATTGATGTGTTCTTAAAGATGGGACAGAAAACAGATCCCTGTGTGATTAATTATTTG	180
Db	1591	AATTGATGTGTTCTTAAAGATGGGACAGAAAACAGATCCCTGTGTGATTAATTATTTG	1650
Oy	181	AACGGGATTCAGATTGAAATGAAGTCAACCAAAGTGACATTACCAATGAGAGGAAAAAC	240
Db	1651	AACGGGATTCAGATTGAAATGAAGTCA-CAAAGTGACATTACCAATGAGAGGAAAAAC	1708
Oy	241	AGACGAGAAATCTTGATGGCTTCAACAAGACATGTGAAC	278
Db	1710	AGACGAGAAATCTTGATGGCTTCAACAAGACATGTGAAC	1747

RESULT 9  
US-09-439-313-313  
: Sequence 313, Application US/09439313  
: Patent No. 6329505  
: GENERAL INFORMATION:  
: APPLICANT: Xu, Jiangchun  
: APPLICANT: Dillon, David C.

APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan Louise  
 APPLICANT: Jiang Yugu  
 APPLICANT: Reed, Steven G.  
 APPLICANT: Kalos, Michael  
 APPLICANT: Fanger, Gary  
 APPLICANT: Retter, Mark  
 APPLICANT: Solk, John  
 APPLICANT: Day, Craig  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C9  
 CURRENT APPLICATION NUMBER: US/09/439,313  
 CURRENT FILING DATE: 1999-11-12  
 NUMBER OF SEQ ID NOS: 575  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 313  
 LENGTH: 718  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(718)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-439-313-313  
 Query Match 86.7%; Score 241; DB 4; Length 718;  
 Best Local Similarity 98.6%; Pred. No. 2.2e-71;  
 Matches 274; Conservative 0; Mismatches 1; Indels 3; Gaps 3

QY	1	CAGGAAACACAAAAGGAAGCA	CACAGATCCCTGGAGAAATGCCGGCCGCAATCTTG	GG	60
QY	231	CAGGAAACACAAAAGGAAGCA <th>CACAGATCCCTGGAGAAATGCCGGCCGCAATCTTG</th> <td>GG</td> <td>290</td>	CACAGATCCCTGGAGAAATGCCGGCCGCAATCTTG	GG	290
Db	61	TCATCGATGAGCCTCGCCCTGTG <td>CTGCTCCGCTTGAGGAAAGCATTGAAATG</td> <td>120</td> <td></td>	CTGCTCCGCTTGAGGAAAGCATTGAAATG	120	
QY	291	TCATCGATGAGCCTCGCCCTGTG <td>CTGCTCCGCTTGAGGAAAGCATTGAAATG</td> <td>350</td> <td></td>	CTGCTCCGCTTGAGGAAAGCATTGAAATG	350	
Db	121	AATTGATGTGTTCTTAAAGATGGG <td>CAGGAAAAACAGATCCTGTGTGATATATTAATG</td> <td>180</td> <td></td>	CAGGAAAAACAGATCCTGTGTGATATATTAATG	180	
QY	351	AATTGATGTGTTCTTAAAGAT	GGCAGGAAAAACAGATCCTGTGTGATATATTAATG	409	
Db	181	AACGGGATTACAGATTTGAAATG <td>AGTCACCCAAAGTAGCATTTACCAATGAGAGAAAAC</td> <td>240</td> <td></td>	AGTCACCCAAAGTAGCATTTACCAATGAGAGAAAAC	240	
QY	410	AACGGGATTACAGATTTGAAATG <td>AGTCACCAAGTAGCATTTACCAATGAGAGAAAAC</td> <td>468</td> <td></td>	AGTCACCAAGTAGCATTTACCAATGAGAGAAAAC	468	
Db	241	AGACGAGAAATCTTGATGCTTAC <td>CAAGACATGCAAC</td> <td>278</td> <td></td>	CAAGACATGCAAC	278	
QY	469	AGACGAGAAATCTTGATGCTTAC <td>CAAGACATGCAAC</td> <td>505</td> <td></td>	CAAGACATGCAAC	505	

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RESULT 10
US-09-352-616A-313
Sequence 313, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, David C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42768
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:

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Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 AGCATTCACATGAGAGAAACAGAGAAATCTTGATGCTTCACAAAGCATGCA 277  
Db 301 AGCATTCACATGAGAGAAACAGAGAAATCTTGATGCTTCACAAAGCATGCA 242

QY 278 C 278  
Db 241 C 241

## RESULT 14

US-09-232-149A-287/C  
Sequence 287, Application US/09232149A  
Patent No. 6465611  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C6  
CURRENT APPLICATION NUMBER: US/09/232.149A  
NUMBER OF SEQ ID NOS: 338  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 287  
LENGTH: 301  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-232-149A-287

Query Match 21.9%; Score 61; DB 4; Length 301;  
Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 AGCATTCACATGAGAGAAACAGAGAAATCTTGATGCTTCACAAAGCATGCA 277  
Db 301 AGCATTCACATGAGAGAAACAGAGAAATCTTGATGCTTCACAAAGCATGCA 242

QY 278 C 278  
Db 241 C 241

## RESULT 15

US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BERT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-F18  
US-08-232-463-14

Query Match 12.9%; Score 36; DB 1; Length 7218;  
Best Local Similarity 2.2%; Pred. No. 0.064;  
Matches 6; Conservative 156; Mismatches 106; Indels 0; Gaps 0;

QY 2 AGAAGACACAAAAGAGACAGACAGATCCCTGGAGAAATGCCGCCCATCTTGGGT 61

Db 1326 RRR 1267

QY 62 CATGATGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121

Db 1266 RRR 1207

QY 122 ATGATGTGTCTTAAAGATGCGACGAGAAACAGATCCTGTGTGATATTATTGA 181

Db 1206 RRR 1147

QY 182 ACGGATTACAGATTGAATGAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAG 241

Db 1146 RRR 1087

QY 242 GACGAGAAATCTTGATGCTTCACAG 269

Db 1086 RRR 1059

Search completed: February 1, 2004, 10:41:49  
Job time: 53 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 09:50:21 ; Search time 222 Seconds  
(without alignments)  
4563.904 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278

Sequence: 1 caggaagcacaagaagc.....ggttcacaagatcgaac 278

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: Published\_Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/PCR\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCRUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

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12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

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15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	266	95.7	812	9	US-09-780-669-471
C 3	266	95.7	812	9	US-09-822-827-471
C 4	266	95.7	812	10	US-09-895-793-471
C 5	266	95.7	812	10	US-09-895-814-471
C 6	266	95.7	812	13	US-10-144-678A-471
C 7	266	95.7	812	13	US-10-294-025-471
C 8	266	95.7	812	15	US-10-012-896-471
C 9	266	95.7	812	15	US-10-010-940-471
C 10	266	95.7	875	11	US-09-957-708-3
C 11	266	95.7	2229	9	US-09-759-143-469
C 12	266	95.7	2229	9	US-09-780-669-469
C 13	266	95.7	2229	9	US-09-822-827-469
C 14	266	95.7	2229	10	US-09-895-793-469
C 15	266	95.7	2229	10	US-09-895-814-469

C 16	266	95.7	2229	13	US-10-144-678A-469	Sequence 469, App
C 17	266	95.7	2229	13	US-10-294-025-469	Sequence 469, App
C 18	266	95.7	2229	14	US-10-012-896-469	Sequence 469, App
C 19	266	95.7	2229	15	US-10-010-940-469	Sequence 469, App
C 20	266	95.7	2229	15	US-09-759-143-470	Sequence 470, App
C 21	266	95.7	2229	9	US-09-780-669-470	Sequence 470, App
C 22	266	95.7	2229	10	US-09-822-827-470	Sequence 470, App
C 23	266	95.7	2229	10	US-09-895-793-470	Sequence 470, App
C 24	266	95.7	2229	13	US-09-895-814-470	Sequence 470, App
C 25	266	95.7	2229	13	US-10-144-678A-470	Sequence 470, App
C 26	266	95.7	2229	13	US-10-294-025-470	Sequence 470, App
C 27	266	95.7	2229	14	US-10-012-896-470	Sequence 470, App
C 28	266	95.7	2229	15	US-10-010-940-470	Sequence 470, App
C 29	266	95.7	2229	15	US-10-205-823-448	Sequence 468, App
C 30	266	95.7	2229	9	US-09-759-143-468	Sequence 468, App
C 31	266	95.7	2229	9	US-09-780-669-468	Sequence 468, App
C 32	266	95.7	2229	9	US-09-822-827-468	Sequence 468, App
C 33	266	95.7	2229	10	US-09-895-793-468	Sequence 468, App
C 34	266	95.7	2229	10	US-09-895-814-468	Sequence 468, App
C 35	266	95.7	2229	13	US-10-144-678A-468	Sequence 468, App
C 36	266	95.7	2229	13	US-10-294-025-468	Sequence 468, App
C 37	266	95.7	2229	14	US-10-012-896-468	Sequence 468, App
C 38	266	95.7	2229	15	US-10-010-940-468	Sequence 468, App
C 39	266	95.7	2229	9	US-09-759-143-690	Sequence 690, App
C 40	266	95.7	2229	9	US-09-780-669-690	Sequence 690, App
C 41	266	95.7	2229	9	US-09-822-827-690	Sequence 690, App
C 42	266	95.7	2229	10	US-09-895-793-690	Sequence 690, App
C 43	266	95.7	2229	10	US-09-895-814-690	Sequence 690, App
C 44	266	95.7	2229	13	US-10-144-678A-690	Sequence 690, App
C 45	266	95.7	2229	13	US-10-294-025-690	Sequence 690, App

## ALIGNMENTS

RESULT 1

US-09-759-143-471/c

Sequence 471, Application US/09759143

Patent No. US2002002248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqun

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

NUMBER OF FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 471

LENGTH: 812

TYPE: DNA

ORGANISM: Homo sapiens

US-09-759-143-471

Query Match 95.7%; Score 266; DB 9; Length 812;

Best Local Similarity 99.6%; Pred. No. 9,7e-76;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;











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QY 61 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTAAGGAGACATTAGAAAATG 120
DB 1557 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTAAGGAGACATTAGAAAATG 1498
QY 121 AATTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCTGTGTAATTTATTTG 180
DB 1497 AATTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCTGTGTAATTTATTTG 1438
QY 181 AACGGGATTCAGATTGGAATGAAGTCAACCAAGATGAGCATTCACATGAGAGAAAAC 240
DB 1437 AACGGGATTCAGATTGGAATGAAGTCA-CAAAGTGAAGCATTCACATGAGAGAAAAC 1379
QY 241 AGACGAGAAAATCTTGATGGCTTCACAAGATGCAAC 278
DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAGATGCAAC 1341

RESULT 12
US-09-780-669-469/c
; Sequence 469, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: McNeill, John
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-469

Query Match 95.7%; Score 266; DB 9; Length 2229;
Best Local Similarity 99.6%; Pred. No. 1.7e-75;
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAGATGCAAC 1341

RESULT 13
US-09-822-827-469/c
; Sequence 469, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.

Query Match 95.7%; Score 266; DB 9; Length 2229;
Best Local Similarity 99.6%; Pred. No. 1.7e-75;
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAGCACAAGGAGACAGAGATCCCTGGAGAAATGCCCGCCGCATCTTGGG 60
DB 1617 CAGGAGCACAAGGAGACAGAGATCCCTGGAGAAATGCCCGCCGCATCTTGGG 1558
QY 61 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTAAGGAGACATTAGAAAATG 120
DB 1557 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTAAGGAGACATTAGAAAATG 1498
QY 121 AATTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCTGTGTAATTTATTTG 180
DB 1497 AATTGATGTGTTCTCTTAAAGGATGGGACAGAAAACAGATCTGTGTAATTTATTTG 1438
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DB 1437 AACGGGATTCAGATTGGAATGAAGTCA-CAAAGTGAAGCATTCACATGAGAGAAAAC 1379
QY 241 AGACGAGAAAATCTTGATGGCTTCACAAGATGCAAC 278
DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAGATGCAAC 1341

RESULT 14
US-09-895-793-469/c
; Sequence 469, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
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RESULT 15  
US-09-895-814-469/c  
Sequence 469, Application US/09895814  
Publication No. US20020193296A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Devin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yaser A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hurst, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carloa  
APPLICANT: Foy, Teresa  
APPLICANT: Panger, Gary R.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

Search completed: February 1, 2004, 10:45:36  
Job time : 223 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 09:35:11 ; Search time 1315 Seconds  
(without alignments)  
5138.133 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278  
Sequence: 1 caggaagcacaagaagc.....ggcttcacaagacatgcaac 278

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: em\_esthum:\*  
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7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
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25: em\_gss\_rod:\*  
26: em\_gss\_png:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	43.6	15.7	489	BG224987	BG224987 kp52h05.Y
4	41.4	14.9	1016	BX442677	BX442677 BX442677

C	5	41	14.7	1098	13	BX435460	BX435460
C	6	40	14.4	1029	29	CNS02GLH	ALI96478 Tetraodon
C	7	38.2	13.7	1051	29	CC241440	CC241440 CH261-96M
C	8	37.4	13.5	393	12	BI541137	BI541137 454735 MA
C	9	37	13.3	206	9	AA815526	AA815526 VP28C02.X
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C	11	37	13.3	397	14	CA752332	CA752332 UI-M-FOO-
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C	13	36.8	13.2	804	29	B2819014	B2819014 PUGCO697B
C	14	36.8	13.2	880	29	B2819018	B2819018 PUGCO697D
C	15	36.6	13.2	906	28	AA540309	AA540309 ENTCT15TR
C	16	36.4	13.1	1201	13	BX461310	BX461310 BX461310
C	17	36	12.9	547	10	BE494725	BE494725 WHE1257_A
C	18	36	12.9	1201	13	BX398121	BX398121 BX398121
C	19	35.8	12.9	748	28	AQ329159	AQ329159 nbxb0044B
C	20	35.8	12.9	1185	29	CC259009	CC259009 CH261-164
C	21	35.8	12.9	1201	29	CNS010CB	AL052030 Drosophila
C	22	35.4	12.7	632	28	A2523825	A2523825 223PBH05
C	23	35.4	12.7	658	29	AG014902	AG014902 Homo sapi
C	24	35.4	12.7	669	29	AG014901	AG014901 Homo sapi
C	25	35.4	12.7	683	28	B2082789	B2082789 11a17C06
C	26	35.4	12.7	907	10	BF970829	BF970829 602271468
C	27	35.4	12.7	926	29	CNS0081M	AL052030 Drosophila
C	28	35.4	12.7	990	29	CC211728	CC211728 CH261-74K
C	29	35.4	12.7	1201	9	AL536976	AL536976 AL536976
C	30	35.2	12.7	618	29	B2797594	B2797594 PUGDT71TD
C	31	35.2	12.7	953	29	CC384522	CC384522 PUBBM10TD
C	32	35	12.6	630	12	BM392983	BM392983 50071-2-4
C	33	35	12.6	630	12	BM394450	BM394450 50072-2-4
C	34	35	12.6	689	28	AQ588780	AQ588780 CITB1-EI-
C	35	35	12.6	892	28	A2539947	A2539947 ENTBD61TF
C	36	35	12.6	913	28	A2530814	A2530814 ENTBE20TF
C	37	35	12.6	1201	13	BX386038	BX386038 BX386038
C	38	34.8	12.5	660	29	AG046758	AG046758 Pan trogl
C	39	34.8	12.5	729	29	AG001111	AG001111 Homo sapi
C	40	34.8	12.5	834	28	A2689940	A2689940 ENTLM12TF
C	41	34.8	12.5	919	28	A2547772	A2547772 ENTFQ09TF
C	42	34.6	12.4	243	29	AG220724	AG220724 Lotus jap
C	43	34.6	12.4	341	28	AQ070955	AQ070955 HS 2174 A
C	44	34.4	12.4	395	28	AO188363	AO188363 HS 3228 A
C	45	34.4	12.4	529	12	BI324783	BI324783 rkb0910.Y

#### ALIGNMENTS

RESULT 1  
LOCUS BF373406 167 bp mRNA EST 24-NOV-2000  
DEFINITION IL2-FT0159-070800-120-H01 FT0159 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF373406  
VERSION BF373406.1 GI:11335431  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 167)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.V.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE  
PUBMED 20202663  
COMMENT 10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,

Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICP Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?fil=IL2&ct=IL2-PT0159-070800-120-H01&f3=2000-08-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 167.  
Location/Qualifiers

## FEATURES

source

1.167  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="PT0159"  
/note="Organ: prostate tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## BASE COUNT

47 a 38 c 49 g 33 t

## ORIGIN

Query Match 59.4%; Score 165; DB 10; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.3e-35;  
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCCGCGCATCTTGGG 60  
Db 3 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCCGCGCATCTTGGG 62  
Qy 61 TCATCGATGAGCTCGCCCTGCTGCTGGTCCCGCTTGTGAGGAGACATTAGAAATG 120  
Db 63 TCATCGATGAGCTCGCCCTGCTGCTGGTCCCGCTTGTGAGGAGACATTAGAAATG 122  
Qy 121 AATTGATGTGTTCTTAAGAGTGGGAGGAAACAGATCCTGTT 165  
Db 123 AATTGATGTGTTCTTAAGAGTGGGAGGAAACAGATCCTGTT 167

RESULT 2 402 bp mRNA linear EST 12-SEP-1997  
LOCUS AA578773  
DEFINITION nt24a04.s1 NCI\_CGAP\_P1 Homo sapiens cDNA clone IMAGE:953262, mRNA  
sequence.  
AA578773  
VERSION AA578773.1 GI:2356957  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 402)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuqui, M.D.,  
, Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdip/image/image.html  
Insert Length: 565 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 373.  
Location/Qualifiers  
1.402  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:953262"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP P1"  
/note="Vector: pAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st  
strand cDNA was primed with oligo(dT)17 on 50 ng of  
DNase-treated, total cellular RNA obtained from 5,000-10,  
000 microdissected, histologically normal prostate  
epithelial cells. Double-stranded cDNA was ligated to  
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with  
an adaptor-specific primer, and the resulting PCR product  
subcloned into pAMP10 by the UDG-cloning method (Life  
Technologies). Average insert size is 600 bp. NOTE: Not  
directionally cloned. This library was constructed by  
David Krizman."

## BASE COUNT

128 a 86 c 84 g 104 t

## ORIGIN

Query Match 42.8%; Score 119; DB 9; Length 402;  
Best Local Similarity 95.7%; Pred. No. 1.9e-22;  
Matches 133; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 140 GGATGGCGAGAAACAGATCCCTGTTGGATTTATTTGAAACGGATTACAGATTGA 199  
Db 1 GGTCGACACAGAAACAGATCCCTGTTGGATTTATTTGAAACGGATTACAGATTGA 60  
Qy 200 AATGAAGTCCCAAGAGACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATG 259  
Db 61 AATGAAGTCA-CAAAGTACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATG 119  
Qy 260 GCTTCAACAGACATGCAAC 278  
Db 120 GCTTCAACAGACATGCAAC 138

RESULT 3 489 bp mRNA linear EST 09-MAY-2001  
LOCUS BG224987  
DEFINITION kp52h05.y1 TBN95TM-SPF Strongyloides stercoralis cDNA 5' similar  
to WP:COB811.7 CE01477 HYPOTHETICAL 37.7 KD PROTEIN COB811.7 IN  
CHROMOSOME II ; mRNA sequence.  
BG224987  
VERSION BG224987.1 GI:12712542  
KEYWORDS EST.  
SOURCE Strongyloides stercoralis  
ORGANISM Strongyloides stercoralis  
REFERENCE 1 (bases 1 to 489)  
AUTHORS McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J., Wylie,T.,  
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,  
, Gibbons,M., Rittner,B., Bennett,J., Franklin,C., Taagarelshvili,R.,  
, Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe  
, M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,  
, Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and  
Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
The library was constructed by Dr. Thomas Nutman and colleagues of





```

Oy 157 GATCCTGTTGGACATATTTATTTGACGCGATTCACAGATTGAATGACATGACCAAGT 216
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 542 AAKARKKKKKAKKAAARKKAKKMAAAAVKKKKKAAAAMGAAAAAMKKKAAAAAMAK 483

Oy 217 GAGCATTTCCAAATGAGAGAAAACAGACGAGAAAATCTTGATGCTTCACAGACA 272
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 KAAAMKAAAMMMAMMMKAKKAAKMMMAAKMMKMKKMMMMMMKMAAMMMKMM 427

RESULT 6
CNS02GLH 1029 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
13710 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL196478.1 GI:7834628
GSS: genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS Roest Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Flzames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
REFERENCE
AUTHORS Roest Crollius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C.,
Flzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
10899143
3 (bases 1 to 1029)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a larges
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
Source
1..1029
/organism="Tetraodon nigroviridis"
/mol_type="Genomic DNA"
/db_xref="taxon:99883"
/clone="137L10"
/clone_11b="G"
/note="Genoscope sequence ID : COAG137DF05LP1-end : T7"

BASE COUNT 300 a 66 c 233 g 211 t 219 others

ORIGIN
Query Match 14.4% Score 40; DB 29; Length 1029;
Best Local Similarity 41.3% Pred. NO. 2.6;
Matches 62; Conservative 27; Mismatches 61; Indels 0; Gaps 0;

Oy 103 GAGGACATTTAGAAAATGAATGATGATGTTCTTTAAGAGATGGCAGAGAAAACAGATCCT 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 839 DAASAKAKMTAKCAKAKGKWKGTATTTATTAACAAAAMASGTGATTTAMAMATTTGT 898

Oy 163 GTTGCGATATTTATTTGACGCGATTCACAGATTGGAATGAAGTCACCAAGTGACAT 222

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[illegible]

VERSION	BI541137.1	GI:15382249
KEYWORDS	EST	
SOURCE	Bos taurus (cow)	
ORGANISM	Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	
REFERENCE	Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Cnaas,E., Wray,J.E., White,J., Cho,Y., Fahrenkrug,S.C., Bennett, G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chilko-McKown,C.G., Pettes,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W. Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)	
TITLE	JOURNAL MEDLINE PUBMED	21180013 11282978
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCOCAGTCAGCAG Plate: 119 row: I column: 22 Seq primer: ATTTAGGTGACACTAATTAG. Location/Qualifiers 1..393 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_id="MARC 1BOV" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."	
FEATURES	BASE COUNT	112 a 77 c 116 g 87 t 1 others
ORIGIN	Query Match	13.5%; Score 37.4; DB 12; Length 393;
	Best Local Similarity	58.0%; Pred. No. 11;
	Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;	
OY	82 TGCCGTGGTCCCGCTTGATGAGGAAGACATTAGAATAATGATGTGTTCTTAAGG	141
Dd	217 TGCCCTNAGAGGTTTGAAGGTAATACATTGGGAAACAATATATGAAACAATGAAGG	276
OY	142 ATGGGCAGAAAACAGATCTGTTGTGATATTATTGAAACGGATTACAG	193
Dd	277 CTATATCTGGGAACAGCTGTACTGAGGAAACCTTTCAGAAATGATTAACAG	328
RESULT_9	AAB15526	206 bp mRNA linear EST 13-FEB-1998
LOCUS	AAB15526	vp28c02.r1 Barstead mouse proximal colon MBLR86 Mus musculus cDNA clone IMAGE:1077986 5', mRNA sequence.
DEFINITION	AAB15526	
ACCESSION	AAB15526.1	GI:2885122
VERSION	AAB15526.1	GI:2885122
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muride; Murinae; Mus.	
REFERENCE	Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	
AUTHORS		

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project	Unpublished	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. WGI:592282
Seq primer: -28ml3 rev2 ET from Amersham.	Location/Qualifiers	
1. 206	/organism="Mus musculus"	
	/mol_type="mRNA"	
	/strain="FVB/N"	
	/db_xref="taxon:10090"	
	/clone="IMAGE:1077986"	
	/dev_stage="7 day juvenile"	
	/lab_host="DH10B"	
	/clone_1db="Barstead mouse proximal colon MFLR6"	
	/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5', TGTTAGCATCTGACAGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT 3'); double-stranded cDNA was ligated to Eco RI adaptors [AATCGCATCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library constructed by Bob Barstead."	
BASE COUNT	110 a	25 c 29 g 42 t
ORIGIN		
Query Match	13.3%	Score 37; DB 9; Length 206;
Best Local Similarity	56.0%;	Pred. No. 11;
Matches	70; Conservative	0; Mismatches 55; Indels 0; Gaps 0;
QY	127	TGTTCTCTTAAGAGTGGCGAGAAAACAGATCTGTTGGATATTATTGAACGGG 186
DB	66	TGTTCTCACTCAAGATGGCGACAGATGAAGAACTCATGTGAATCTATAAAATGAC 125
QY	187	ATTACAGATTGGAATGATGACCAAGAGAGCATTCACCAATGAGAGAAAACAGACGA 246
DB	126	CTTTGCCCTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 185
QY	247	GAAAA 251
DB	186	AAAAA 190
RESULT 10		
LOCUS	AA710451	384 bp mRNA linear EST 24-DEC-1997
DEFINITION	vt42ef07.r1 Barstead mouse proximal colon MFLR6 Mus musculus cDNA	
ACCESSION	AA710451	
VERSION	AA710451.1	GI:2720369
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus (house mouse)	
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 384) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepec,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	

TITLE  
JOURNAL  
COMMENT

The WashU-HMNI Mouse EST Project  
Unpublished  
Contact: Marra M/Mouse EST Project  
WashU-HMNI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
WGI: 631677

Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 363.

## FEATURES

## source

Location/Qualifiers

1. 384  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1165765"  
/dev\_stage="7 day juvenile"  
/lab\_host="DH10B"  
/clone\_lib="Barestead mouse proximal colon MPRB6"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer 15',  
TGTTCACATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT  
311; double-stranded cDNA was ligated to Eco RI adaptors  
(AATTCGATCTTG), digested with Not I and cloned into the  
Not I and Eco RI sites of the modified pT733 vector.  
Library constructed by Bob Barestead."

BASE COUNT  
ORIGIN

164 a 67 c 65 g 88 t

Query Match 13.3%; Score 37; DB 9; Length 384;  
Best Local Similarity 56.0%; Pred. No. 14;  
Matches 70; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 127 TGTTCCTTAAGAGTGGAGGAGAAACAGATCTGTGTGATTTATTTAAGCGG 186  
DB 245 TGTCTACCTCAAGCATGGCGAGATMAAGAACTCATGTGAATCTTAATAAATGAC 304  
QY 187 ATTCAGATTGAATGATGACCAAAAGTGAATTCATGAGAGAGAAACAGAGA 246  
DB 305 CTTTGCCCTTTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364  
QY 247 GAAAA 251  
DB 365 AAAAA 369

RESULT 11  
CA752332 397 bp mRNA linear EST 27-NOV-2002  
LOCUS CA752332  
DEFINITION UI-M-FOO-cdo-m-15-0-UI-r1 NIH BMAP\_F00 Mus musculus cDNA clone  
IMAGE: 6831256 5', mRNA sequence.  
ACCESSION CA752332.1 GI:25582740  
VERSION CA752332.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 397)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
The following repetitive elements were found in this cDNA  
sequence: 217-329, >POLY\_A\$Simple\_repeat  
Seq primer: pyx-5.

## FEATURES

## source

Location/Qualifiers

1. 397  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE: 6831256"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 12.5dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_F00"  
/note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pyx-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TGAAGAGGC. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,  
program coordinator."

BASE COUNT 175 a 62 c 70 g 90 t

## ORIGIN

Query Match 13.3%; Score 37; DB 14; Length 397;  
Best Local Similarity 50.9%; Pred. No. 14;  
Matches 88; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 79 CTGTGCTGTGCTCCGCTGTGTGAGGAGAGACATTAGAAATGAATGATGTCTTAA 138  
DB 97 CTGGGGTTGATCTCTCTATGTGGGCAAGTTCAAAGTTAAATGATTTTCTTTT 156  
QY 139 AGGATGGGCAAGAAACAGATCTCTGTGTGATTTATTTGAACGGATTTACAGATTG 198  
DB 157 ACTCTTGCCCAAAATTGAGAGATGCTGTGAATATCATTTTGAACCTGTGTAATATATG 216  
QY 199 AATGAAAGTCACCAAGTGAAGTTCATTCATGAGAGAGAAACAGAGAGAAA 251  
DB 217 AAGAGAGAAAAAAG 269

RESULT 12  
BF299229 811 bp mRNA linear EST 04-MAY-2001  
LOCUS BF299229  
DEFINITION 053PBH06 Pb cDNA #20, Charles Yewell and Jane Carlton Plasmodium  
BERGHEI CDNA 3', mRNA sequence.  
ACCESSION BF299229.1 GI:13952844  
VERSION BF299229.1  
KEYWORDS EST.  
SOURCE Plasmodium berghei  
ORGANISM Plasmodium berghei  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
1 (bases 1 to 811)  
REFERENCE Carlton, J.M.-R. and Dame, J.B.  
TITLES The plasmodium vivax and P. berghei gene sequence tag projects  
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)  
JOURNAL Contact: Dame JB  
COMMENT Department of Pathobiology, College of Veterinary Medicine  
University of Florida



Best Local Similarity 51.2%; Pred. No. 19;  
Matches 86; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 99 GAGGGAAGACATTAGAAATGAATTGATGTTCTTAAAGATGGCGCGGAAAACAGA 158  
Db 517 GAGGATAGGAAGCTACATATTAAGAAAAAGTGAATTAAGATGAGGGGTATTAAGGA 458

QY 159 TCCTGTTGGATGATTTATTTGAACGGATTACGATTGAATGAAGTCACCAAGTGA 218  
Db 457 ATCTAGAACCAATCTAGTTTATTTTACCTTAACCTTAACACGCCAAATAG 398

QY 219 GCATTACCAATGAGAGAAAACAGACGAGAAATCTTGATGCTTCAC 266  
Db 397 TCTGAACCAATTGAGATGACATGATAACAGTATTGCAATTAC 350

RESULT 15  
AZ540309 906 bp DNA linear GSS 14-NOV-2000  
LOCUS ENTCC215TR Entamoeba histolytica Sheared DNA Entamoeba histolytica  
DEFINITION genomic, genomic survey sequence.  
ACCESSION AZ540309  
VERSION AZ540309.1 GI:11146986  
KEYWORDS GSS.

SOURCE Entamoeba histolytica  
ORGANISM Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (Bases 1 to 906)  
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.  
TITLE Determination of clone end sequences from Entamoeba histolytica  
JOURNAL HM1:IMSS sheared DNA library

COMMENT Unpublished  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: b.loftus@igr.org  
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared  
DNA library  
Seq primer: M13-Reverse  
Class: Shotgun  
High quality sequence start: 89  
High quality sequence stop: 243.  
Location/Qualifiers  
1. .906

FEATURES  
Source /organism="Entamoeba histolytica"  
/mol\_type="genomic DNA"  
/strain="HM1:IMSS"  
/db\_xref="taxon:5759"  
/clone\_id="Entamoeba histolytica Sheared DNA"  
/note="Vector: pHO51; Site 1: Bst I; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark,  
C.G., and Diamond, J.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + i method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barell, Oxford University Press, 1999)."

BASE COUNT 410 a 115 c 137 g 244 t  
ORIGIN

Query Match 13.2%; Score 36.6; DB 28; Length 906;  
Best Local Similarity 58.9%; Pred. No. 22;  
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 168 GGATATTATTGACGGATTACGATTGAATGAAGTCACCAAGTGAAGCATTTACA 227

Db 217 GGAATAATTAATTAATAATGAAAAAATATGAACGACTTCAATGAATGAACCATATTA 276

QY 228 ATAGAGGAAAAACAGACGAGAAAAATCTGATGGCTTCACAAAGCATG 274  
Db 277 ATGAGAGTAAAAAATATGTAAGAAAAATCAGGAGTCATRGAACATG 323

Search completed: February 1, 2004, 10:40:53  
Job time : 1319 secs







KW	Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
OS	Homo sapiens.
XX	MO200173032-A2.
XX	04-OCT-2001.
PD	
XX	27-MAR-2001; 2001WO-US09919.
PF	
XX	27-MAR-2001; 2000US-0536857.
XX	09-MAY-2000; 2000US-0568100.
PR	13-MAY-2000; 2000US-0570737.
PR	13-JUN-2000; 2000US-0593793.
PR	27-JUN-2000; 2000US-0605783.
PR	10-AUG-2000; 2000US-0636215.
PR	29-AUG-2000; 2000US-0651236.
PR	06-SEP-2000; 2000US-0657279.
PR	02-OCT-2000; 2000US-0679426.
PR	10-OCT-2000; 2000US-0685166.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX	
DR	WPI; 2001-639232/73.
XX	
PT	New human prostate-specific polypeptides and polynucleotides useful for
PT	the diagnosis and treatment of cancer, especially prostate cancer -
PS	Claim 1; Page 386-387; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC	antibodies raised against the polypeptides (or antigenic epitopes
CC	derived from them) and antigen-presenting cells expressing the
CC	polypeptides. The antibodies are useful for detecting the presence of
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC	the antigen-presenting cells are useful for stimulating and/or expanding
CC	T cells specific for a tumour protein, and for inhibiting the development
CC	of cancer especially prostate cancer. Compositions comprising the
CC	polynucleotide and/or polypeptide are useful for stimulating an immune
CC	response, and for treating cancer. The oligonucleotide is useful for
CC	detecting cancer. The present sequence is a prostate specific
CC	polynucleotide of the invention.
XX	
XX	Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
XX	
Query Match	95.7%; Score 266; DB 22; Length 812;
Best Local Similarity	99.6%; Pred. No. 4.7e-76;
Matches	277; Conservative 0; Mismatches 0; Indels 1; Gaps 1
QY	1 CAGGAGACAAAGAGACACAGATCCCTGGAGAAATGCCGCGCATTTGGG 60
DB	562 CAGGAGACAAAGAGAGACACAGATCCCTGGAGAAATGCCGCGCATTTGGG 503
QY	61 TCATGATGAGGCTCGCCCTGGCTGGTCCCGCTTGAGGAGAGACATTAGAAATG 120
DB	502 TCATGATGAGGCTCGCCCTGGCTGGTCCCGCTTGAGGAGAGACATTAGAAATG 443
QY	121 AATTGATGTGTTCTTAAAGATGGGAGAAACAGATCCTGTTGTGATATTATTTG 180
DB	442 AATTGATGTGTTCTTAAAGATGGGAGAAACAGATCCTGTTGTGATATTATTTG 383
QY	181 AACGGATTACAGATTGGAATGAATGACCAAAAGTAGACATTACCAATGAGAGAAAAC 240
DB	382 AACGGATTACAGATTGGAATGAATGACCAAAAGTAGACATTACCAATGAGAGAAAAC 324
QY	241 AGACGAGAAATCTTGATGGCTTCAACAGACATGCAAC 278
DB	323 AGACGAGAAATCTTGATGGCTTCAACAGACATGCAAC 286

ID	AAH93806/c	standard; cDNA; 812 BP.
XX	AAH93806/c	
AC	AAH93806;	
DT	04-OCT-2001	(first entry)
DE	Human prostate-specific cDNA sequence P710P #4.	
KM	Human; prostate cancer; prostate-specific; diagnosis; vaccine;	
KW	cytostatic; gene therapy; metastasis; ss.	
OS	Homo sapiens.	
PN	MO200151633-A2.	
PD	19-JUL-2001.	
PF	16-JAN-2001; 2001WO-US01574.	
PR	14-JAN-2000; 2000US-0483672.	
XX	(CORI-) CORIXA CORP.	
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;	
P1	Kalos MD, Fanger GF, Day CH, Retter MM, Stolk JA, Skeiky YAM;	
P1	Mang A, Meagher MJ;	
XX	WPI; 2001-425873/45.	
DR	New polynucleotide encoding a prostate-specific protein, for	
XX	diagnosing, monitoring and treating prostate cancer in a patient and	
PT	for use in vaccines -	
PT	Claim 1; Page 365; 543pp; English.	
PS	The present invention describes polynucleotide sequences (I) which encode	
XX	prostate-specific proteins (II). (I) and (II) have cytostatic activity,	
CC	and can be used in vaccine production and gene therapy. (II), (II),	
CC	antibodies to (II), fusion proteins comprising (II), and isolated	
CC	T cells prepared using (I) or (II) are used treat cancer in a patient.	
CC	(I) and the antibodies are also used in the detection of cancer in a	
CC	patient. The cancer that is diagnosed or treated is particularly	
CC	prostate cancer. (I) and (II) can be used in vaccines. The antibodies or	
CC	(I) can be used for monitoring the progression of cancer in a patient.	
CC	(I) and (II) can also be used to improve diagnostic and therapeutic	
CC	methods for prostate cancer. They can indicate the level of metastasis	
CC	as well as the prostate volume. AAH9357 to AAH9394 and AMO115 to	
CC	AMO138 represent polynucleotide and amino acid sequences used in the	
CC	exemplification of the present invention.	
SQ	Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;	
Query Match	95.7%; Score 266; DB 22; Length 812;	
Best Local Similarity	99.6%; Pred. No. 4.7e-76;	
Matches 277; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
OY	1 CAGGAAGCACAAAAGAAGCACAAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGG	60
Dd	562 CAGGAAGCACAAAAGAAGCACAAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGG	503
OY	61 TCATCATGAGCCCTTCGCCCTGTGCTGCTGCTCCGCTTGTAAGGGAAGCAATTAGAAATG	120
Dd	502 TCATCATGAGCCCTTCGCCCTGTGCTGCTGCTCCGCTTGTAAGGGAAGCAATTAGAAATG	443
OY	121 AATTGATGTGTTCTTAAAGATGGGAGAAAAACAGATCCCTGTTGGATATTATTATTTG	180
Dd	442 AATTGATGTGTTCTTAAAGATGGGAGAAAAACAGATCCCTGTTGGATATTATTATTTG	383
OY	181 AACGGGATTACAGATTGAAATGAATGCACCNAAGTAGACATTACCAATGAGAGAAAAAC	240



Db 502 TCATCGATGAGCCTCGCCCTGCTGCTGCCCTGTGTGAGGAGACATTGAAAATG 443  
Qy 121 AATTGATGTGTTCTTAAAGATGGGAGAGAAAACAGATCTGTGTGATATTATTG 180  
Db 442 AATTGATGTGTTCTTAAAGATGGGAGAGAAAACAGATCTGTGTGATATTATTG 383  
Qy 181 AACGGGATTACAGATTGAAATGAAGTCCAAAGTGAGCATTTACCAATGAGAGAAAAC 240  
Db 382 AACGGGATTACAGATTGAAATGAAGTCA-CAAAGTGAGCATTTACCAATGAGAGAAAAC 324  
Qy 241 AGACGAGAAAATCTTGATGGCTTCACAGACATGCAAC 278  
Db 323 AGACGAGAAAATCTTGATGGCTTCACAGACATGCAAC 286

## RESULT 7

AAF86949/c  
ID AAF86949 standard; cDNA; 812 BP.

AAF86949;

06-JUL-2001 (first entry)

Human P710P inventive antigen coding sequence SEQ ID NO: 345.

Human; mouse; immunotherapy; cancer; leukemia; WTI; Wilm's tumour gene;  
chromosome 11p13; zinc finger transcription factor; ss.

Homo sapiens.

MO200125273-A2.

12-APR-2001.

04-OCT-2000; 2000MO-US27465.

04-OCT-1999; 99US-0157459.

(CORI-) CORIXA CORP.

Skeiky YAM, Xu J, Cheever MA, Reed SG;

WPI; 2001-328324/34.

Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
used in the diagnosis and treatment of malignant diseases e.g. leukemia

and cancer associated with WTI

Disclosure; Page 220; 228pp; English.

The present invention describes compositions comprising peptides derived  
from the Wilm's tumour protein WTI and methods for their use in treating  
malignant diseases. Peptides derived from both the murine and human WTI  
proteins are provided. The human WTI gene is found on chromosome 11p13,  
and the protein was shown to be a zinc finger transcription factor. The  
immunogenic peptides of the invention are particularly useful in the  
diagnosis and treatment of cancer and leukemia. The present sequence is  
a coding sequence used in the exemplification of the invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 95.7%; Score 266; DB 22; Length 812;

Best Local Similarity 99.6%; Pred. No. 4.7e-76;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCCGCGCCATCTTGGG 60  
Db 562 CAGGAGCACAAGAGAGAGACAGAGATCCCTGGAGAAATGCCCGCGCCATCTTGGG 503  
Qy 61 TCATCGATGAGCCTGCGCTGTGCTGCTGCTGTGAGGAGAGACATTAGAAATG 120  
Db 502 TCATCGATGAGCCTGCGCTGTGCTGCTGCTGTGAGGAGAGACATTAGAAATG 443

Qy 121 AATTGATGTGTTCTTAAAGATGGGAGAGAAAACAGATCTGTGTGATATTATTG 180  
Db 442 AATTGATGTGTTCTTAAAGATGGGAGAGAAAACAGATCTGTGTGATATTATTG 383  
Qy 181 AACGGGATTACAGATTGAAATGAAGTCCAAAGTGAGCATTTACCAATGAGAGAAAAC 240  
Db 382 AACGGGATTACAGATTGAAATGAAGTCA-CAAAGTGAGCATTTACCAATGAGAGAAAAC 324  
Qy 241 AGACGAGAAAATCTTGATGGCTTCACAGACATGCAAC 278  
Db 323 AGACGAGAAAATCTTGATGGCTTCACAGACATGCAAC 286

## RESULT 8

ABL95270/c  
ID ABL95270 standard; cDNA; 812 BP.

ABL95270;

19-JUL-2002 (first entry)

Human P710P cDNA sequence SEQ ID NO 471.

Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

gene therapy; gene; ss.

Homo sapiens.

US2002022248-A1.

21-FEB-2002.

12-JAN-2001; 2001US-0759143.

25-FEB-1997; 97US-0806099.

01-AUG-1997; 97US-0904804.

09-FEB-1998; 98US-0020956.

25-FEB-1998; 98US-0030607.

14-JUL-1998; 98US-0115453.

23-SEP-1998; 98US-0159812.

15-JAN-1999; 99US-0232149.

09-APR-1999; 99US-028946.

13-JUL-1999; 99US-0352616.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

14-JAN-2000; 2000US-0483672.

27-MAR-2000; 2000US-0536857.

09-MAY-2000; 2000US-0568100.

12-MAY-2000; 2000US-0570737.

13-JUN-2000; 2000US-0593793.

27-JUN-2000; 2000US-0605783.

10-AUG-2000; 2000US-0636215.

29-AUG-2000; 2000US-0651236.

06-SEP-2000; 2000US-0657279.

02-OCT-2000; 2000US-0679426.

10-OCT-2000; 2000US-0685166.

(XUJ/) XU J.  
(DIL/) DILON D C.  
(MITC/) MITCHAM J L.  
(HARL/) HARLOCKER S L.  
(JIAN/) JIANG Y.  
(KALO/) KALOS M D.  
(FANG/) FANGER G R.  
(RETT/) RETTER M W.  
(STOL/) STOLK J A.  
(DAYC/) DAY C H.  
(VEDV/) VEDVICK T S.  
(CART/) CARTER D.  
(LISX/) LI S X.  
(WANG/) WANG A.  
(SKEI/) SKEIKY Y A W.  
(HEPL/) HEPLER W T.









PR 29-AUG-2000; 2000US-0651236.  
PR 06-SEP-2000; 2000US-0657279.  
PR 02-OCT-2000; 2000US-0679426.  
PR 10-OCT-2000; 2000US-0685166.

(CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

PT New human prostate-specific polypeptides and polynucleotides useful for  
XX the diagnosis and treatment of cancer, especially prostate cancer -

PS Claim 1; Page 385; 579pp; English.

XX The invention relates to isolated prostate-specific  
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,  
CC antibodies raised against the polypeptides (or antigenic epitopes  
CC derived from them) and antigen-presenting cells expressing the  
CC polypeptides. The antibodies are useful for detecting the presence of  
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and  
CC the antigen-presenting cells are useful for stimulating and/or expanding  
CC T cells specific for a tumour protein, and for inhibiting the development  
CC of cancer especially prostate cancer. Compositions comprising the  
CC polynucleotide and/or polypeptide are useful for stimulating an immune  
CC response, and for treating cancer. The oligonucleotide is useful for  
CC detecting cancer. The present sequence is a prostate specific  
XX polynucleotide of the invention.

XX Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Query Match 95.7%; Score 266; DB 22; Length 2229;

Best Local Similarity 99.6%; Pred. No. 7.6e-76;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAGACAAAGAGAGACAGAGATCCCTGGAGAAATGCCGGCCGCATCTTGGG 60

Db 1617 CAGGAGACAAAGAGAGACAGAGATCCCTGGAGAAATGCCGGCCGCATCTTGGG 1558

QY 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGGAGAGACATTGAAATG 120

Db 1557 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGGAGAGACATTGAAATG 1498

QY 121 AATTGATGTGTCTCTTAAGAGATGGGACAGAAACAGATCTGTGTGATATTATTG 180

Db 1497 AATTGATGTGTCTCTTAAGAGATGGGACAGAAACAGATCTGTGTGATATTATTG 1438

QY 181 AACGGATTACAGATTGAATGAAGTACCAAAAGTACATTCATGAGAGAAAC 240

Db 1437 AACGGATTACAGATTGAATGAAGTCA-CAAAGTAGCATTTACCAATGAGAGAAAC 1379

QY 241 AGACGAGAAATCTTGATGCTTCACAAACATGCAAC 278

Db 1378 AGACGAGAAATCTTGATGCTTCACAAACATGCAAC 1341

Search completed: February 1, 2004, 09:53:28  
Job time : 190 secs